



<140> Thomas, Susan Margaret
<120> COMPOSITION AND METHOD FOR DETECTING MUTAGENS
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<140> US 09/603,448
<141> 2000-06-26

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<170> PatentIn version 3.1

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Ser Asn Arg Val Met Ser Thr Leu Glu Glu Leu Ser Pro Arg Val Glu
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Ile Tyr Ser Ile Asp Glu Ala Phe Cys Asp Leu Thr Gly Val Arg Asn
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Cys Arg Asp Leu Thr Asp Phe Gly Arg Glu Ile Arg Ala Thr Val Leu
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Gln Arg Thr His Leu Thr Val Gly Val Gly Ile Ala Gln Thr Lys Thr
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Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
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Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
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Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
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Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
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Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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His Pro Ser Ala Thr Tyr Phe Leu Arg Val Ser Gly Ser Ser Met Glu
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Asp Gly Arg Ile His Asp Gly Asp Val Leu Val Val Asp Arg Ser Leu
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Thr Ala Ser His Gly Ser Ile Val Val Ala Cys Ile His Asn Glu Phe
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Thr Val Lys Arg Leu Leu Leu Arg Pro Arg Pro Cys Leu Met Pro Met
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Asn Lys Asp Phe Pro Val Tyr Tyr Ile Asp Pro Asp Asn Glu Ser Val
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50 55 60

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85 90 95

Gln Tyr Ser Ile Asp Glu Leu Phe Val Asp Cys Lys Gly Ile Thr Ala
100 105 110

Ala Met Ser Leu Asp Ala Phe Gly Arg Gln Leu Arg Glu Glu Val Arg
115 120 125

Arg His Thr Thr Leu Val Cys Gly Val Gly Ile Ala Arg Thr Lys Thr
130 135 140

Leu Ala Lys Leu Cys Asn His Ala Ala Lys Thr Trp Pro Ala Thr Gly

145

150

155

160

Gly Val Val Ala Leu Asp Asp Gly Ala Arg Leu Lys Lys Leu Met Ser
165 170 175

Ile Leu Pro Val Ala Glu Val Trp Gly Val Gly His Arg Thr Glu Lys
180 185 190

Ala Leu Ala Thr Met Gly Ile Lys Thr Val Leu Asp Leu Ala Arg Ala
195 200 205

Asp Thr Arg Leu Ile Arg Lys Thr Phe Gly Val Val Leu Glu Arg Thr
210 215 220

Val Arg Glu Leu Arg Gly Glu Ala Cys Phe Ser Leu Glu Glu Asn Pro
225 230 235 240

Pro Ala Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Gln Arg Val
245 250 255

Glu Thr Leu Thr Asp Met Gln Gln Ala Val Thr Gly Phe Ala Ala Arg
260 265 270

Ala Ala Glu Lys Leu Arg Asn Glu Arg Gln Tyr Cys Arg Val Ile Ser
275 280 285

Val Phe Ile Arg Thr Ser Pro Tyr Ser Val Arg Asp Thr Gln Tyr Ala
290 295 300

Asn Gln Ala Thr Glu Lys Leu Thr Val Ala Thr Gln Asp Ser Arg Thr
305 310 315 320

Ile Ile Gln Ala Ala Gln Ala Ala Leu Ala Arg Ile Trp Arg Glu Asp
325 330 335

Ile Ala Tyr Ala Lys Ala Gly Val Met Leu Ala Asp Phe Ser Gly Lys
340 345 350

Glu Ala Gln Leu Asp Leu Phe Asp Ser Ala Thr Pro Ser Ala Gly Ser
355 360 365

Glu Ala Leu Met Ala Val Leu Asp Gly Ile Asn Arg Arg Gly Lys Asn
370 375 380

Gln Leu Phe Phe Ala Gly Gln Gly Ile Asp Asn Ser Phe Ala Met Arg

385

390

395

400

Arg Gln Met Leu Ser Pro Asp Tyr Thr Thr Asp Trp Arg Ser Ile Pro
405 410 415

Ile Ala Thr Ile Lys
420

<210> 13
<211> 74
<212> PRT
<213> Enterobacteriaceae

<400> 13

Met Cys Ile Ala Gln Tyr Ile Tyr Val Arg Leu Ala Val Asn Leu Pro
1 5 10 15

Thr Pro Glu Thr Tyr Asp Glu Leu Gln Arg Ala Tyr Asp Phe Phe Asn
20 25 30

Glu Lys Leu Phe Ser Asn Glu Leu Pro Pro Cys Leu Ile Thr Leu Gln
35 40 45

Arg Glu Lys Arg Thr Tyr Gly Tyr Cys Ser Phe Lys Arg Phe Val Gly
50 55 60

Arg Glu Ser Gly Tyr Thr Val Asp Glu Ile
65 70

<210> 14
<211> 1990
<212> DNA
<213> Escherichia coli

<400> 14
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ggacactgag aaagcagaaaa gccaacaaac actatataata gcgttcgttg gcagctgaag 180
cagcactaca tatagtagag aacctgtaaa acttgccaac ctgaccataa cagcgatact 240
gtataaataaa acagtttattt ggaagatcgc tatgaaggtc gatatttttg aaagctccgg 300
cgccagccgg gtacacagca tccctttta tctgcaaaga atttctgcgg ggttccccag 360
cccgccccag ggctatgaaa agcaggagtt aaacctgcat gagtattgtg ttcgtcaccc 420
ttcagcaact tacttcctgc gggttctgg ctcgtcaatg gaagatggcc gcatccatga 480

tggtgacgta ctgggtgtgg atcgctcgct gacggccagc cacggctcaa tcgttagtcgc 540
ctgcatccat aatgaattta ccgtgaagcg actactgctg aggcccagac cctgcctgat 600
gccgatgaac aaagattttc ctgtgtacta cattgacccg gataatgaga gcgttgaat 660
ctggggagtg gttacgcatt cccttacgt gcatccggta tgtttgcgt gattgatgtc 720
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ggcctgaaaa tgggcgatcc gtacttcaa gtcagaccca taatcgagcg tcataacatc 900
gctattttta gctctaatta cactcttat gcctccatgt cgcccccgtt cgccggccgt 960
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ggcgccagac tgaagaaatt aatgagcatc ctgcccgttg cgaaagtctg gggcgtcggc 1260
catcgtagag agaaagcact cgccacaatg gggatcaaaa cggtgctgga tttagccagg 1320
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ttgcgcggcg aggcttgctt cagcctggaa gaaaaccctc ctgcgaagca gcagattgtt 1440
gtgtcgcgct cattcgccca acgcgtagaa accctgacgg acatgcagca ggctgtcacc 1500
ggatttgcag cgccgcgcagc taaaaactg cgtaatgaga ggcaatactg ccgcgtcata 1560
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gaggcttaa tggctgttct tggatgtata aaccggcgtg gaaagaacca gcttttttt 1860
gcaggccagg gcatcgataa ctcccttgcc atgcgtcgac agatgttgc acctgattac 1920
acgacagact ggccgtcaat accaatagcc accatcaaatt aattaccggc gccgtacccg 1980
ggcccctcgaa 1990

<210> 15
<211> 146
<212> PRT
<213> Escherichia coli

<400> 15

Met Lys Val Asp Ile Phe Glu Ser Ser Gly Ala Ser Arg Val His Ser
1 5 10 15

Ile Pro Phe Tyr Leu Gln Arg Ile Ser Ala Gly Phe Pro Ser Pro Ala
20 25 30

Gln Gly Tyr Glu Lys Gln Glu Leu Asn Leu His Glu Tyr Cys Val Arg
35 40 45

His Pro Ser Ala Thr Tyr Phe Leu Arg Val Ser Gly Ser Ser Met Glu
50 55 60

Asp Gly Arg Ile His Asp Gly Asp Val Leu Val Val Asp Arg Ser Leu
65 70 75 80

Thr Ala Ser His Gly Ser Ile Val Val Ala Cys Ile His Asn Glu Phe
85 90 95

Thr Val Lys Arg Leu Leu Leu Arg Pro Arg Pro Cys Leu Met Pro Met
100 105 110

Asn Lys Asp Phe Pro Val Tyr Tyr Ile Asp Pro Asp Asn Glu Ser Val
115 120 125

Glu Ile Trp Gly Val Val Thr His Ser Leu Ile Glu His Pro Val Cys
130 135 140

Leu Arg
145

<210> 16
<211> 420
<212> PRT
<213> Escherichia coli

<400> 16

Met Phe Ala Leu Ile Asp Val Asn Gly Met Tyr Ala Ser Cys Glu Gln
1 5 10 15

Ala Phe Arg Pro Asp Leu Ala Asn Arg Ala Val Ala Val Leu Ser Asn
20 25 30

Asn Asp Gly Asn Ile Val Ala Arg Asn Tyr Leu Ala Lys Lys Ala Gly
35 40 45

Leu Lys Met Gly Asp Pro Tyr Phe Lys Val Arg Pro Ile Ile Glu Arg

50

55

60

His Asn Ile Ala Ile Phe Ser Ser Asn Tyr Thr Leu Tyr Ala Ser Met
65 70 75 80

Ser Ala Arg Phe Ala Ala Val Val Glu Ser Leu Ala Ser His Val Glu
85 90 95

Gln Tyr Ser Ile Asp Glu Leu Phe Val Asp Cys Lys Gly Ile Thr Ala
100 105 110

Ala Met Ser Leu Asp Ala Phe Gly Arg Gln Leu Arg Glu Glu Val Arg
115 120 125

Arg His Thr Thr Leu Val Cys Gly Val Gly Ile Ala Arg Thr Lys Thr
130 135 140

Leu Ala Lys Leu Cys Asn His Ala Ala Lys Thr Trp Pro Ala Thr Gly
145 150 155 160

Gly Val Val Ala Leu Asp Asp Gly Ala Arg Leu Lys Lys Leu Met Ser
165 170 175

Ile Leu Pro Val Ala Glu Val Trp Gly Val Gly His Arg Thr Glu Lys
180 185 190

Ala Leu Ala Thr Met Gly Ile Lys Thr Val Leu Asp Leu Ala Arg Ala
195 200 205

Asp Thr Arg Leu Ile Arg Lys Thr Phe Gly Val Val Leu Glu Arg Thr
210 215 220

Val Arg Glu Leu Arg Gly Glu Ala Cys Phe Ser Leu Glu Glu Asn Pro
225 230 235 240

Pro Ala Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Gln Arg Val
245 250 255

Glu Thr Leu Thr Asp Met Gln Gln Ala Val Thr Gly Phe Ala Ala Arg
260 265 270

Ala Ala Glu Lys Leu Arg Asn Glu Arg Gln Tyr Cys Arg Val Ile Ser
275 280 285

Val Phe Ile Arg Thr Ser Pro Tyr Ser Val Arg Asp Thr Gln Tyr Ala

290

295

300

Asn Gln Ala Thr Glu Lys Leu Thr Val Ala Thr Gln Asp Ser Arg Thr
305 310 315 320

Ile Ile Gln Ala Ala Gln Ala Leu Ala Arg Ile Trp Arg Glu Asp Ile
325 330 335

Ala Tyr Ala Lys Ala Gly Val Met Leu Ala Asp Phe Ser Gly Lys Glu
340 345 350

Ala Gln Leu Asp Leu Phe Asp Ser Ala Thr Pro Ser Ala Gly Ser Glu
355 360 365

Ala Leu Met Ala Val Leu Asp Gly Ile Asn Arg Arg Gly Lys Asn Gln
370 375 380

Leu Phe Phe Ala Gly Gln Gly Ile Asp Asn Ser Phe Ala Met Arg Arg
385 390 395 400

Gln Met Leu Ser Pro Asp Tyr Thr Thr Asp Trp Arg Ser Ile Pro Ile
405 410 415

Ala Thr Ile Lys
420

<210> 17
<211> 2574
<212> DNA
<213> *Salmonella typhimurium*

<220>
<221> CDS
<222> (211)..(630)
<223>

<220>
<221> CDS
<222> (633)..(1901)
<223>

<400> 17
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ccggaaaatt tacaaaaccc ataatttcaa ctgagagaga aacttacaaa cgaagcgacg
aagatttaaa cagtcgttagc gactccggta tcttgcgcgc atgttcaaat aacactactg 120
tatataaaaa cagtattcga ggtatggatt atg gaa ttt ttc aga cct aca gag 180
234

Met Glu Phe Phe Arg Pro Thr Glu			
1	5		
ttg cgc gaa att att cct ctc cca ttt ttc agt tac tta gtg ccg tgt		282	
Leu Arg Glu Ile Ile Pro Leu Pro Phe Ser Tyr Leu Val Pro Cys			
10	15	20	
gga ttc ccc agc ccc gcg gcg gac tac att gag cag cgt atc gat ctt		330	
Gly Phe Pro Ser Pro Ala Ala Asp Tyr Ile Glu Gln Arg Ile Asp Leu			
25	30	35	40
aat gag ttg ctc gtt tct cat ccc agc tca aca tat ttt gtc aaa gcc		378	
Asn Glu Leu Leu Val Ser His Pro Ser Ser Thr Tyr Phe Val Lys Ala			
45	50	55	
tcg ggg gat tca atg att gaa gca ggc atc agc gac ggt gac ctg ctg		426	
Ser Gly Asp Ser Met Ile Glu Ala Gly Ile Ser Asp Gly Asp Leu Leu			
60	65	70	
gtg gtg gat agc tca cgg aac gct gac cac ggt gac att gta att gcg		474	
Val Val Asp Ser Ser Arg Asn Ala Asp His Gly Asp Ile Val Ile Ala			
75	80	85	
gca att gaa gga gag ttc acc gta aaa cgg ttg cag ttg cgc ccg aca		522	
Ala Ile Glu Gly Glu Phe Thr Val Lys Arg Leu Gln Leu Arg Pro Thr			
90	95	100	
gtg cag tta atc ccc atg aac ggc gcc tat cga cct ata cct gtc ggc		570	
Val Gln Leu Ile Pro Met Asn Gly Ala Tyr Arg Pro Ile Pro Val Gly			
105	110	115	120
agt gaa gac acg ctc gac ata ttc ggg gtg gtg acc ttt atc att aaa		618	
Ser Glu Asp Thr Leu Asp Ile Phe Gly Val Val Thr Phe Ile Ile Lys			
125	130	135	
gcg gtc agt tga tt atg ttc gcg ctc tgc gat gtt aat agc ttt tac		665	
Ala Val Ser Met Phe Ala Leu Cys Asp Val Asn Ser Phe Tyr			
140	145	150	
gcc tcc tgc gaa acg gtc ttt cgt cct gat tta tgt ggc cga ccg gtg		713	
Ala Ser Cys Glu Thr Val Phe Arg Pro Asp Leu Cys Gly Arg Pro Val			
155	160	165	
gtg gtg tta tca aac aat gat ggc tgc gtt atc gcg tgt agc gcc gag		761	
Val Val Leu Ser Asn Asn Asp Gly Cys Val Ile Ala Cys Ser Ala Glu			
170	175	180	
gcg aaa cag ctc ggt atc gca cca ggt gag cca tac ttc aaa cag aaa		809	
Ala Lys Gln Leu Gly Ile Ala Pro Gly Glu Pro Tyr Phe Lys Gln Lys			
185	190	195	
gaa cgc ttc cgg cga tcc ggt gtt gtc ttc agc agt aat tac gag		857	
Glu Arg Phe Arg Arg Ser Gly Val Val Cys Phe Ser Ser Asn Tyr Glu			
200	205	210	
ctt tac gct gat atg tcg aac cgg gta atg acc aca ctc gag gag atg		905	
Leu Tyr Ala Asp Met Ser Asn Arg Val Met Thr Thr Leu Glu Glu Met			
215	220	225	230
gtg ccg cgg gta gaa att tac agc att gat gag gcc ttt tgt gat ctg		953	

Val Pro Arg Val Glu Ile Tyr Ser Ile Asp Glu Ala Phe Cys Asp Leu			
235	240	245	
acg ggg gta cga aac tgc cggt gat ctg aca gat ttc ggg cgc gag ata			1001
Thr Gly Val Arg Asn Cys Arg Asp Leu Thr Asp Phe Gly Arg Glu Ile			
250	255	260	
aga gcg acg gtc ctg aag cgcc acg cac ctg act gtc ggt gta ggc att			1049
Arg Ala Thr Val Leu Lys Arg Thr His Leu Thr Val Gly Val Gly Ile			
265	270	275	
gcc cag acg aaa acc ctt gcc aag ctg gct aac cat gct gcg aaa aag			1097
Ala Gln Thr Lys Thr Leu Ala Lys Leu Ala Asn His Ala Ala Lys Lys			
280	285	290	
tgg cag cgc cag acc gac ggg gtg gtt gac ttg tcg aac atc gat cgc			1145
Trp Gln Arg Gln Thr Asp Gly Val Val Asp Leu Ser Asn Ile Asp Arg			
295	300	305	310
cag cgt cgg ctg ctg gcc ctg ata ccc gtg gag gat gtc tgg ggt gtc			1193
Gln Arg Arg Leu Leu Ala Leu Ile Pro Val Glu Asp Val Trp Gly Val			
315	320	325	
ggc agg cgc atc agt aag aag ctc aat gcc ctg ggc atc aag act gct			1241
Gly Arg Arg Ile Ser Lys Lys Leu Asn Ala Leu Gly Ile Lys Thr Ala			
330	335	340	
ctc gat ctc tct gaa caa agt acc tgg atc atc agg aaa cac ttc aat			1289
Leu Asp Leu Ser Glu Gln Ser Thr Trp Ile Ile Arg Lys His Phe Asn			
345	350	355	
gtc gtg ctg gag cgt acc gtg aga gag ctt cgc gga gag cca tgt ctg			1337
Val Val Leu Glu Arg Thr Val Arg Glu Leu Arg Gly Glu Pro Cys Leu			
360	365	370	
gag ctc gaa gag ttt gcg ccg gca aag cag gaa atc gtt tgt agt cgc			1385
Glu Leu Glu Glu Phe Ala Pro Ala Lys Gln Glu Ile Val Cys Ser Arg			
375	380	385	390
tct ttc ggc gag cgg gtc aca gac tat gag gaa atg cgc cag gct gtt			1433
Ser Phe Gly Glu Arg Val Thr Asp Tyr Glu Glu Met Arg Gln Ala Val			
395	400	405	
tac agc tac gct gcg cgc gca gaa aaa ctc cgc ggc gag cac cag			1481
Tyr Ser Tyr Ala Ala Arg Ala Ala Glu Lys Leu Arg Gly Glu His Gln			
410	415	420	
tac tgc cgt ttc att tca aca ttc gtc aaa aca tca ccc ttt gcc ctg			1529
Tyr Cys Arg Phe Ile Ser Thr Phe Val Lys Thr Ser Pro Phe Ala Leu			
425	430	435	
aac gag ccc tac tac ggt aac agc gcc gcg gtg acg ctt ctc acc ccc			1577
Asn Glu Pro Tyr Tyr Gly Asn Ser Ala Ala Val Thr Leu Leu Thr Pro			
440	445	450	
acg cag gat tca cgt gac att atc aat gcg gct gtg aaa tgc ctg gat			1625
Thr Gln Asp Ser Arg Asp Ile Ile Asn Ala Ala Val Lys Cys Leu Asp			
455	460	465	470
aaa ata tgg cgc gac ggc cat cgc tac cag aaa gcg ggg gtg atg ctg			1673

Lys Ile Trp Arg Asp Gly His Arg Tyr Gln Lys Ala Gly Val Met Leu			
475	480	485	
ggt gac ttc ttc agt cag ggc gta gcg caa ctc aac ctt ttc gac gat		1721	
Gly Asp Phe Phe Ser Gln Gly Val Ala Gln Leu Asn Leu Phe Asp Asp			
490	495	500	
aac gcg ccg cgc gcc ggt agt gcg aag ttg atg gaa gta ctg gac cat		1769	
Asn Ala Pro Arg Ala Gly Ser Ala Lys Leu Met Glu Val Leu Asp His			
505	510	515	
ctt aac gca aaa gac ggg aag ggg acg ctg tac ttc gcc ggg cag ggg		1817	
Leu Asn Ala Lys Asp Gly Lys Gly Thr Leu Tyr Phe Ala Gly Gln Gly			
520	525	530	
atg tcg caa cag tgg gct atg aag cga gaa atg ctt tcg cct cgg tac		1865	
Met Ser Gln Gln Trp Ala Met Lys Arg Glu Met Leu Ser Pro Arg Tyr			
535	540	545	550
acc aca aga tac tct gat cta ctg cgt gtt aag taa cttgtgcgat		1911	
Thr Thr Arg Tyr Ser Asp Leu Leu Arg Val Lys			
555	560		
caatgcctga gatgggtgcc aaatcatccc cgttctctaa ccgggtttgg tcgcacaaga		1971	
tcacaggaac ctctcacgat gagttgtgc gatcaatgcc tgagatggtt gccaaatcat		2031	
ccccgttctc taaccggttt tggtcgcaca agatcacagg aacctctcac gatgaggcgc		2091	
atgtatcctg gtttacgaca tcagaaaatg tggcgcgtt attgcccggc aggcgttgt		2151	
agacgtcact tatttacgccc aggtttcagc cgtacgcaca ggcataataaaaagat		2211	
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ctatgttcag ttaaccatgc gttatgggtt gtgcgggtt atacaaactt atctgaagta		2331	
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acgacgaaaaa tcactgggtt agtaaaaatgg tttttttttt cttttttttt cttttttttt		2511	
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ttc		2574	

<210> 18
 <211> 139
 <212> PRT
 <213> *Salmonella typhimurium*

<400> 18

Met Glu Phe Phe Arg Pro Thr Glu Leu Arg Glu Ile Ile Pro Leu Pro			
1	5	10	15

Phe Phe Ser Tyr Leu Val Pro Cys Gly Phe Pro Ser Pro Ala Ala Asp

20

25

30

Tyr Ile Glu Gln Arg Ile Asp Leu Asn Glu Leu Leu Val Ser His Pro
35 40 45

Ser Ser Thr Tyr Phe Val Lys Ala Ser Gly Asp Ser Met Ile Glu Ala
50 55 60

Gly Ile Ser Asp Gly Asp Leu Leu Val Val Asp Ser Ser Arg Asn Ala
65 70 75 80

Asp His Gly Asp Ile Val Ile Ala Ala Ile Glu Gly Glu Phe Thr Val
85 90 95

Lys Arg Leu Gln Leu Arg Pro Thr Val Gln Leu Ile Pro Met Asn Gly
100 105 110

Ala Tyr Arg Pro Ile Pro Val Gly Ser Glu Asp Thr Leu Asp Ile Phe
115 120 125

Gly Val Val Thr Phe Ile Ile Lys Ala Val Ser
130 135

<210> 19
<211> 422
<212> PRT
<213> *Salmonella typhimurium*

<400> 19

Met Phe Ala Leu Cys Asp Val Asn Ser Phe Tyr Ala Ser Cys Glu Thr
1 5 10 15

Val Phe Arg Pro Asp Leu Cys Gly Arg Pro Val Val Val Leu Ser Asn
20 25 30

Asn Asp Gly Cys Val Ile Ala Cys Ser Ala Glu Ala Lys Gln Leu Gly
35 40 45

Ile Ala Pro Gly Glu Pro Tyr Phe Lys Gln Lys Glu Arg Phe Arg Arg
50 55 60

Ser Gly Val Val Cys Phe Ser Ser Asn Tyr Glu Leu Tyr Ala Asp Met
65 70 75 80

Ser Asn Arg Val Met Thr Thr Leu Glu Glu Met Val Pro Arg Val Glu
85 90 95

Ile Tyr Ser Ile Asp Glu Ala Phe Cys Asp Leu Thr Gly Val Arg Asn
100 105 110

Cys Arg Asp Leu Thr Asp Phe Gly Arg Glu Ile Arg Ala Thr Val Leu
115 120 125

Lys Arg Thr His Leu Thr Val Gly Val Gly Ile Ala Gln Thr Lys Thr
130 135 140

Leu Ala Lys Leu Ala Asn His Ala Ala Lys Lys Trp Gln Arg Gln Thr
145 150 155 160

Asp Gly Val Val Asp Leu Ser Asn Ile Asp Arg Gln Arg Arg Leu Leu
165 170 175

Ala Leu Ile Pro Val Glu Asp Val Trp Gly Val Gly Arg Arg Ile Ser
180 185 190

Lys Lys Leu Asn Ala Leu Gly Ile Lys Thr Ala Leu Asp Leu Ser Glu
195 200 205

Gln Ser Thr Trp Ile Ile Arg Lys His Phe Asn Val Val Leu Glu Arg
210 215 220

Thr Val Arg Glu Leu Arg Gly Glu Pro Cys Leu Glu Leu Glu Glu Phe
225 230 235 240

Ala Pro Ala Lys Gln Glu Ile Val Cys Ser Arg Ser Phe Gly Glu Arg
245 250 255

Val Thr Asp Tyr Glu Glu Met Arg Gln Ala Val Tyr Ser Tyr Ala Ala
260 265 270

Arg Ala Ala Glu Lys Leu Arg Gly Glu His Gln Tyr Cys Arg Phe Ile
275 280 285

Ser Thr Phe Val Lys Thr Ser Pro Phe Ala Leu Asn Glu Pro Tyr Tyr
290 295 300

Gly Asn Ser Ala Ala Val Thr Leu Leu Thr Pro Thr Gln Asp Ser Arg
305 310 315 320

Asp Ile Ile Asn Ala Ala Val Lys Cys Leu Asp Lys Ile Trp Arg Asp
325 330 335

Gly His Arg Tyr Gln Lys Ala Gly Val Met Leu Gly Asp Phe Phe Ser
340 345 350

Gln Gly Val Ala Gln Leu Asn Leu Phe Asp Asp Asn Ala Pro Arg Ala
355 360 365

Gly Ser Ala Lys Leu Met Glu Val Leu Asp His Leu Asn Ala Lys Asp
370 375 380

Gly Lys Gly Thr Leu Tyr Phe Ala Gly Gln Gly Met Ser Gln Gln Trp
385 390 395 400

Ala Met Lys Arg Glu Met Leu Ser Pro Arg Tyr Thr Thr Arg Tyr Ser
405 410 415

Asp Leu Leu Arg Val Lys
420

<210> 20
<211> 2138
<212> DNA
<213> *Salmonella typhimurium*

<400> 20
gatatccaaa ctgaccccaa aaggtaggg ggagaatgtc cttgccat aaaactgttc 60
ccggtttgtt atttctctgc ccgtgttaa aagttgaaag ttgataactt tgcataaaa 120
tgccgttatac atatataactg tataaatgta cagctaagga gaggcattaa tgtcactaaa 180
acctatgaaa tcagccctg acaccaaaga aactatccct ttctttggcg agctcgtaacc 240
cgcaggtttc cctagccctg ctgctgggtg ggaagaggct gaacttaatc ttcatacgct 300
ggtggttact catccagcca gcacgtactt cttgcgcgtg acaggtgact ccatgcagga 360
tgctcgata cattctggtg acgtgctggt ggtgatcgc tcagaaactc cagagcaggg 420
tagtattgtt gttgccagca tcgacaacga attacagtc aagaaactca tcttgcggcc 480
acgtccatgc cttatgccga tgaacccggc atacccacct atctattttg accctgaaag 540
taacgacgtt gaaatttggg gtgtggtgac ttactcatta atgaagcaca aaaaatgtat 600
ggcctgatcg acattaattc ctgctactgt gcctgcgagc aagcattcag gcccgatctt 660
gctggtaaac ccgtagtagt tttgtcaaac aatgatgcca gctgcatacg ccgtaacaag 720
caggcgaaag cccttggtat aaaaatgggc gagccattct ttaaaaatcaa agatctcata 780
gaacggaaca atgtcgctgt tttcagttca aactatgccc tttattccgc atttagttcc 840

cggtttgcat	ctgttataga	gtcactgact	ccgcgtagct	cagtgtattc	aatcgatgaa	900
cttgggttg	atgccacgaa	tatcactggt	ttaatgactc	ttgatgccta	tggccgcatt	960
ttgcgagaag	aggtacagcg	tcagacaacg	cttacttgtg	gtgttggat	agcaccgaca	1020
aaaacactcg	cgaaattgtg	ttctcatgtc	tcaaaaacct	atccggcaac	tggcggagtt	1080
gtcgcgctt	atgatgttac	ccgtttagaa	aagctgatgc	ggcttgtgcc	cgttgaagac	1140
gtgtgggtg	ttggcccacg	gctggtaaa	aggcttcggt	ttatggagt	gaaaccgcg	1200
tttcaactat	cctgccttga	tcctgttccg	gtacgaaagc	agttcaatgt	tgtcctttag	1260
cgtaccgtca	gggaactccg	gggggagcct	tgcattggcgc	ttgacgaaaa	tgtgtgatg	1320
aaacagcaaa	tagtcgttcc	ccgctccttc	ggtgagcgg	tcaccaacct	tcatgaaatg	1380
cagcaagcca	taaccgatta	tgcggctcgc	gctggcgaaa	aactccggca	agaaaaaggg	1440
tatgtctctg	taattgggt	ttttatacgc	accagccct	acgcagtaaa	tgtgtacct	1500
tattccaatc	aggctactga	aatgctggtg	actccctcca	acgacagcag	ggatattatt	1560
aatgctgcac	aacgcgcatt	aacggatctg	gaggccagaa	gtccgttatg	ctaaagcagg	1620
tgtgatgctt	tgtgatattc	gcgagcgtga	gcctcaactt	gatttgttca	ctgaatcgcc	1680
ccagtaccgc	aacagtgaaa	atctcatgca	attactggat	actctcaaca	agcagggtag	1740
acacaatttg	tttttgccg	gacaaggtat	aaaccccggt	ttcgcaatga	agagaaatat	1800
gctatcccct	gcataatttga	ctaggctggg	atgatttacc	aaaggtagg	ttaggataag	1860
cccactaacc	atcaaaaaga	cataatttt	ccttggtggt	tcacttcgccc	cccctcactc	1920
gtccggcagc	gcaatttggt	tctcaagggt	acgtgttcaa	aaacagctat	aagattatgg	1980
tcacgcgctg	taagccatgc	cagaactaaa	taaattggat	tttttgcataa	tgaaaatata	2040
gcgacgaacg	ttgcaaaaact	gttttattgc	tacaattccc	cttggcttgg	aaaatacata	2100
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<210> 21

<211> 145

<212> PRT

<213> *Salmonella typhimurium*

<400> 21

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Pro	Phe	Phe	Gly	Glu	Leu	Val	Pro	Ala	Gly	Phe	Pro	Ser	Pro	Ala	Ala
					20				25				30		

Gly Trp Glu Glu Ala Glu Leu Asn Leu His Thr Leu Val Val Thr His
35 40 45

Pro Ala Ser Thr Tyr Phe Leu Arg Val Thr Gly Asp Ser Met Gln Asp
50 55 60

Ala Arg Ile His Ser Gly Asp Val Leu Val Val Asp Arg Ser Glu Thr
65 70 75 80

Pro Glu Gln Gly Ser Ile Val Val Ala Ser Ile Asp Asn Glu Phe Thr
85 90 95

Val Lys Lys Leu Ile Leu Arg Pro Arg Pro Cys Leu Met Pro Met Asn
100 105 110

Pro Ala Tyr Pro Pro Ile Tyr Phe Asp Pro Glu Ser Asn Asp Val Glu
115 120 125

Ile Trp Gly Val Val Thr Tyr Ser Leu Met Lys His Lys Lys Cys Met
130 135 140

Ala
145

<210> 22
<211> 339
<212> PRT
<213> *Salmonella typhimurium*

<400> 22

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Ala Phe Arg Pro Asp Leu Ala Gly Lys Pro Val Val Val Leu Ser Asn
20 25 30

Asn Asp Ala Ser Cys Ile Ala Arg Asn Lys Gln Ala Lys Ala Leu Gly
35 40 45

Ile Lys Met Gly Glu Pro Phe Phe Lys Ile Lys Asp Leu Ile Glu Arg
50 55 60

Asn Asn Val Ala Val Phe Ser Ser Asn Tyr Ala Leu Tyr Ser Ala Phe
65 70 75 80

Ser Ser Arg Phe Ala Ser Val Ile Glu Ser Leu Thr Pro Arg Ser Ser

85

90

95

Val Tyr Ser Ile Asp Glu Leu Trp Phe Asp Ala Thr Asn Ile Thr Gly
100 105 110

Leu Met Thr Leu Asp Ala Tyr Gly Arg Met Leu Arg Glu Glu Val Gln
115 120 125

Arg Gln Thr Thr Leu Thr Cys Gly Val Gly Ile Ala Pro Thr Lys Thr
130 135 140

Leu Ala Lys Leu Cys Ser His Ala Ser Lys Thr Tyr Pro Ala Thr Gly
145 150 155 160

Gly Val Val Ala Leu Asp Asp Val Thr Arg Leu Glu Lys Leu Met Arg
165 170 175

Leu Val Pro Val Glu Asp Val Trp Gly Val Gly Pro Arg Leu Gly Lys
180 185 190

Arg Leu Arg Phe Met Gly Val Glu Thr Ala Phe Gln Leu Ser Cys Leu
195 200 205

Asp Pro Val Arg Val Arg Lys Gln Phe Asn Val Val Leu Glu Arg Thr
210 215 220

Val Arg Glu Leu Arg Gly Glu Pro Cys Met Ala Leu Asp Glu Asn Asp
225 230 235 240

Val Met Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Glu Arg Val
245 250 255

Thr Asn Leu His Glu Met Gln Gln Ala Ile Thr Asp Tyr Ala Ala Arg
260 265 270

Ala Ala Glu Lys Leu Arg Gln Glu Lys Gly Tyr Val Ser Val Ile Gly
275 280 285

Val Phe Ile Arg Thr Ser Pro Tyr Ala Val Asn Asp Val Pro Tyr Ser
290 295 300

Asn Gln Ala Thr Glu Met Leu Val Thr Pro Ser Asn Asp Ser Arg Asp
305 310 315 320

Ile Ile Asn Ala Ala Gln Arg Ala Leu Thr Asp Leu Glu Ala Arg Ser

325

330

335

Pro Leu Cys

<210> 23
 <211> 736
 <212> DNA
 <213> Aequorea victoria

<220>
 <221> CDS
 <222> (14)..(730)
 <223>

<400> 23
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 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
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 cca att ttg gtt gaa tta gat ggt gat gtt aat ggt cac aaa ttt tct 97
 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
 15 20 25
 gtc tcc ggt gaa ggt gaa ggt gat gct act tac ggt aaa ttg acc tta 145
 Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 30 35 40
 aaa ttt att tgt act act ggt aaa ttg cca gtt cca tgg cca acc tta 193
 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 45 50 55 60
 gtc act act ttc ggt tat ggt gtt caa tgt ttt gct aga tac cca gat 241
 Val Thr Thr Phe Gly Tyr Val Gln Cys Phe Ala Arg Tyr Pro Asp
 65 70 75
 cat atg aaa caa cat gac ttt ttc aag tct gcc atg cca gaa ggt tat 289
 His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 80 85 90
 gtt caa gaa aga act att ttt ttc aaa gat gac ggt aac tac aag acc 337
 Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
 95 100 105
 aga gct gaa gtc aag ttt gaa ggt gat acc tta gtt aat aga atc gaa 385
 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 110 115 120
 tta aaa ggt att gat ttt aaa gaa gat ggt aac att tta ggt cac aaa 433
 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
 125 130 135 140
 ttg gaa tac aac tat aac tct cac aat gtt tac atc atg gct gac aaa 481
 Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
 145 150 155
 caa aag aat ggt atc aaa gtt aac ttc aaa att aga cac aac att gaa 529

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu		
160	165	170
gat ggt tct gtt caa tta gct gac cat tat caa caa aat act cca att		577
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile		
175	180	185
ggt gat ggt cca gtc ttg tta cca gac aac cat tac tta tcc act caa		625
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln		
190	195	200
tct gcc tta tcc aaa gat cca aac gaa aag aga gac cac atg gtc ttg		673
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu		
205	210	215
tta gaa ttt gtt act gct gct att acc cat ggt atg gat gaa ttg		721
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu		
225	230	235
tac aaa taa ctgcag		736
Tyr Lys		

<210> 24
 <211> 238
 <212> PRT
 <213> Aequorea victoria

<400> 24

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1	5	10
		15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20	25	30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35	40	45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50	55	60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln		
65	70	75
		80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85	90	95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100	105	110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

115

120

125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235